

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph at page 22, lines 10-14, with the following amended paragraph:

Peptide R27: GPGSRARAAGARGC (SEQ ID NO: 44, corresponds to amino acids 30-43 of SEQ ID NO:9);

Peptide R28: LGHRSDLVRFRC (SEQ ID NO: 45, corresponds to amino acids 57-70 of SEQ ID NO:9);

Peptide R29: CRRARSPHDLSL (SEQ ID NO: 46, corresponds to amino acids 74-85 of SEQ ID NO:9);

Peptide R30: LRPPGSRPVSQPC (SEQ ID NO: 47, corresponds to amino acids 94-107 of SEQ ID NO:9); and

Peptide R31: STWRTVDRLSATA (SEQ ID NO: 48, corresponds to amino acids 123-136 of SEQ ID NO:9).

Please replace the paragraph at page 47, lines 16-18, with the following amended paragraph:

Based on a Clustal W (1.75)-based multiple sequence alignment, SEQ ID NO: 9 (neublastin) was aligned with the amino acid sequences of GDNF (SEQ ID NO: 49), persephin (SEQ ID NO: 50) and neurturin (SEQ ID NO 51). This alignment is illustrated in Table 3.

Please replace the paragraph at page 48, lines 28-33, with the following amended paragraph:

* indicates that one of the following `strong` groups is fully conserved: -STA, NEQK (SEQ ID NO: 52), NHQK (SEQ ID NO: 53), NDEQ (SEQ ID NO: 54), QHRK (SEQ ID NO: 55), MILV (SEQ ID NO: 56), MILF (SEQ ID NO: 57), HY, FYW.

. indicates that one of the following `weaker` groups is fully conserved: -CSA, ATV, SAG, STNK (SEQ ID NO: 58), STPA (SEQ ID NO: 59), SGND (SEQ ID NO: 60), SNDEQK (SEQ ID NO: 61), NDEQHK (SEQ ID NO: 62), NEQHRK (SEQ ID NO: 63), VLIM (SEQ ID NO: 64), HFY.

Please replace the paragraph at page 49, lines 11-13, with the following amended paragraph:

Based on this sequence alignment, neublastin was shown to be a member of the GDNF subfamily of neurotrophic factors (LGLG (SEQ ID NO: 65)-FR(Y/F)CSGSC (SEQ ID NO: 66)-QxCCRP (SEQ ID NO: 67)-SAxxCGC (SEQ ID NO: 68), the GDNF subfamily fingerprint, underlined in Table 3).

Please replace the paragraph at page 68, lines 7-12, with the following amended paragraph:

Peptide R27: GPGSRARAAGARGC (SEQ ID NO: 44, corresponds to amino acids 30-43 of SEQ ID NO: 9);

Peptide R28: LGHRSEDELVRFRFC (SEQ ID NO: 45, corresponds to amino acids 57-70 of SEQ ID NO: 9);

Peptide R29: CRRARSPHDLSL (SEQ ID NO: 46, corresponds to amino acids 74-85 of SEQ ID NO: 9);

Peptide R30: LRPPPGSRPVSQPC (SEQ ID NO: 47, corresponds to amino acids 94-107 of SEQ ID NO: 9); and

Peptide R31: STWRTVDRLSATAAC (SEQ ID NO: 48, corresponds to amino acids 123-136 of SEQ ID NO: 9).

Please insert the following at page 69, line 30:

SEQ ID NO.:44 “Peptide R27”; corresponds to amino acids 30-43 of SEQ ID NO: 9.

SEQ ID NO.:45 “Peptide R28”; corresponds to amino acids 57-70 of SEQ ID NO: 9.

SEQ ID NO.:46 “Peptide R29” corresponds to amino acids 74-85 of SEQ ID NO: 9.

SEQ ID NO.:47 “Peptide R30” corresponds to amino acids 94-107 of SEQ ID NO:9).

SEQ ID NO.:48 “Peptide R31” corresponds to amino acids 123-136 of SEQ ID NO:9.

SEQ ID NO.:49 Amino acid sequence of full length human GDNF from Table 3.

SEQ ID NO.: 50 Amino acid sequence of full length persephin from Table 3.

SEQ ID NO.: 51 Amino acid sequence of full length neurturin from Table 3.

SEQ ID NO.:52 Strong conserved group between neublastin polypeptides.

SEQ ID NO.:53 Strong conserved group between neublastin polypeptides.

SEQ ID NO.:54 Strong conserved group between neublastin polypeptides.

SEQ ID NO.:55 Strong conserved group between neublastin polypeptides.

SEQ ID NO.:56 Strong conserved group between neublastin polypeptides.

SEQ ID NO.:57 Strong conserved group between neublastin polypeptides.

SEQ ID NO.: 58 Weak conserved group between neublastin polypeptides.

SEQ ID NO.:59 Weak conserved group between neublastin polypeptides.

SEQ ID NO.:60 Weak conserved group between neublastin polypeptides.

SEQ ID NO.:61 Weak conserved group between neublastin polypeptides.

SEQ ID NO.:62 Weak conserved group between neublastin polypeptides.

SEQ ID NO.:63 Weak conserved group between neublastin polypeptides.

SEQ ID NO.: 64 Weak conserved group between neublastin polypeptides.

SEQ ID NO.:65 GDNF subfamily fingerprint, from Table 3.

SEQ ID NO.:66 GDNF subfamily fingerprint, from Table 3.

SEQ ID NO.:67 GDNF subfamily fingerprint, from Table 3.

SEQ ID NO.: 68 GDNF subfamily fingerprint, from Table 3.

SEQ ID NO.: 69 nucleotide fragment of persephin aligned with the neublastin primer according to SEQ ID NO:17, from Figure 8.

SEQ ID NO.: 70 nucleotide fragment of neurturin aligned with the neublastin primer according to SEQ ID NO:17, from Figure 8.

SEQ ID NO.: 71 nucleotide fragment of GDNF aligned with the neublastin primer according to SEQ ID NO:17, from Figure 8.

SEQ ID NO.: 72 nucleotide fragment of persephin aligned with the neublastin primer according to SEQ ID NO:18, from Figure 8.

SEQ ID NO.:73 nucleotide fragment of neurturin aligned with the neublastin primer according to SEQ ID NO:18, from Figure 8,

SEQ ID NO.: 74 nucleotide fragment of GDNF aligned with the neublastin primer according to SEQ ID NO:18, from Figure 8.

SEQ ID NO.: 75 neublastin amino acid sequence of Syngene from Figure 14.

SEQ ID NO.:76 hisneublastin amino acid sequence of Syngene from Figure 15.

Please insert the Sequence Listing provided herein, pages 1-34, at the end of the specification.